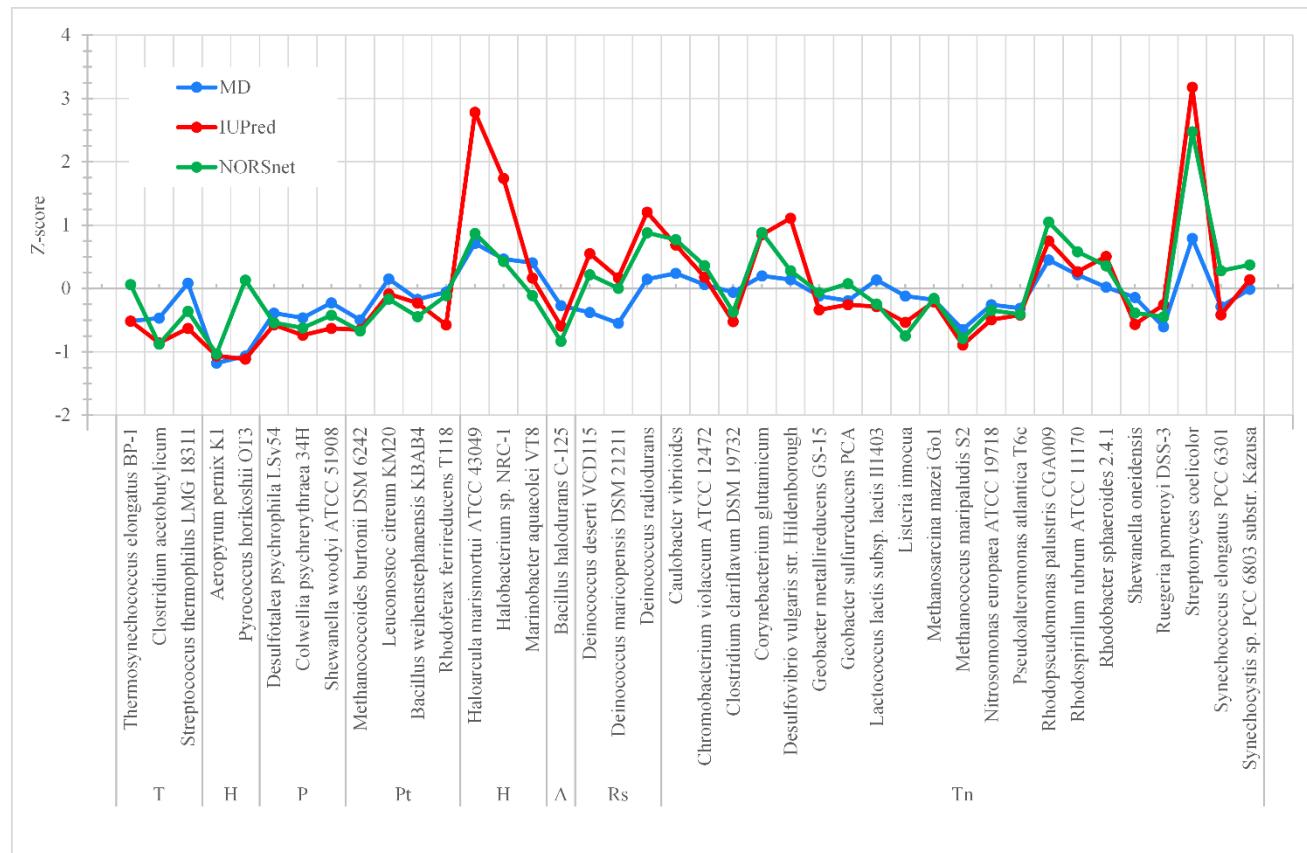


Fig. S4:**Fig. S4: Distribution of disorder content in different organisms for %long50.**

Fractions of proteins with long regions of disorder (here ≥ 50 consecutive residues) were predicted by three prediction methods (MD, NORSnet and IUPred). The raw values are standardized using the Z-scores (Eqn. 1) and the mean and standard deviation (sd) obtained from a population of 1613 prokaryotes calculated for each method (positive: higher than the mean; negative: below the mean; integers +/- N imply $N \cdot sd$ above/below the mean). The taxonomic neighbors section compares the disorder predicted for the closest relatives of the extremophiles. Abbreviations: T, Thermophiles; H, Hyperthermophiles; P, Psychrophiles; Pt, Psychrotolerants; H, Halophiles; A, Ahlkalophla; Rs, Radiation resistent; Tn, Taxonomic neighbors.